In the Specification

Please enter the SEQUENCE LISTING into the specification.

Please amend the paragraph starting on line 1 of page 4 as follows:

Therefore, it is an object of the present invention to provide a consensus sequence for the recognition/interaction of cholesterol comprising

$$-Z-(X)_{0-5}-Y-(X)_{0-5}-Q \text{ (SEQ ID NO:26)}$$

wherein Z represents a neutral and hydrophobic amino acid, such as Leucine or Valine, Y represents a neutral and polar amino acid, such as Tyrosine, Q represents a basic amino acid, such as Arginine or Lysine and X represents any amino acid. The presence of the consensus sequence in a protein infers the likelihood of interaction with cholesterol.

Please amend the paragraph starting on line 9 of page 10 as follows:

In one embodiment, the present invention relates to a minimum amino acid sequence specific for recognition/interaction with cholesterol, namely the amino acid sequence

$$-Z-(X)_{0-5}-Y-(X)_{0-5}-Q \text{ (SEQ ID NO:26)}$$

wherein Z represents a neutral and hydrophobic amino acid, such as Leucine, Valine, Alanine, Isoleucine, Methionine, Phenylalanine and Tryptophan, Y represents a neutral and polar amino acid, such as Tyrosine, Threonine, Serine, Glycine, Glutamine, Cysteine, Asparagine, Q represents a basic amino acid, such as Arginine, Lysine, or arginine, and X represents any amino acids selected from the group consisting of Alanine (Ala, A), Arginine (Arg, R), Asparagine (Asn, N), Aspartic acid (Asp, D), Cystein (Cys, C) Glutamine (Gln, Q), Glutamic acid (Glu, E), Glycine (Gly, G), Histidine (His, H), Isoleucine (Ile, I), Leucine (Leu, L), Lysine (Lys, K), Methionine (Met, M), Phenylalanine (Phe, F), Proline (Pro, P), Serine (Ser, S), Threonine (Thr, T), Tryptophan (Trp, W), Tyrosine (Tyr, Y), and Valine (Val, V).

Please amend the paragraph starting on line 18 of page 47 as follows:

Recent studies by Pikuleva *et al.* (1995, *Arch. Biochem. Biophys.* 322:189-197) with another protein that interacts with cholesterol, the enzyme P450scc, indicated that a Tyrosine in the active site of the P450scc interacts with the side chain of cholesterol. Aligning the P450scc active site amino acid sequence with the carboxy-terminus of PBR indicated that there might be a common amino acid consensus pattern in these two molecules recognizing cholesterol (Table I). This consensus pattern is composed of a neutral and hydrophobic amino acid (Z), such as Leucine or Valine, a neutral and polar amino acid (Y), such as Tyrosine, and a basic amino acid (Q), such as Arginine or Lysine. One to five different amino acids may be placed between these three coding amino acids. Thus, the proposed consensus pattern is **-Z-$(X)_{0-5}$-Y-$(X)_{0-5}$-Q-** (SEQ ID NO:26). Leucine or Valine will interact with the hydrophobic side chain of cholesterol and Tyrosine will interact with the polar 3'OH-group of cholesterol, whereas the Arginine or Lysine may help create a pocket. This hypothesis was tested (Fig. 5). Replacement of Y153 by Serine or R156 by Leucine completely abolished the ability of PBR to take up radiolabeled cholesterol. Mutation and replacement of A147 with Threonine, did not affect cholesterol uptake by bacteria expressing the mutated receptor. Fig. 5 also shows that the wild-type and mutated recombinant receptor proteins were expressed at equal levels upon IPTG induction.

Please amend the paragraph starting on line 14 of page 48 as follows:

In an effort to see whether this putative cholesterol recognition/interaction amino acid consensus pattern is present in other molecules shown or suggested to interact with cholesterol, such as the as apolipoprotein A-1 (Boyle, T. P. and Marotti, K. R., 1992, *Gene* 117, 243-247), caveolin (Murata, M. *et al.* 1995, *Proc. Natl. Aca. Aci. USA* 92, 10339-10343), DBI (Papadopoulos, V. 1993, *Endocr. Rev.* 14, 222-240; Papadopoulos, V. 1998, *Proc. Soc. Exp. Biol. Med.* 217, 130-142), steroidogenesis acute regulatory protein (StAR) (Stocco, D. M. and Clark, B. J. 1996, *Endocr. Rev.* 17, 221-244), hedgehog protein (Porter, J. A. *et al.* 1996, *Science* 274, 255-259), cytochrome P450 C26/25 (Su, P. *et al.* 1990, *DNA Cell Biol.* 9-657-667), annexin II (Harder, T. *et al.* 1997, *Mol. Biol. Cell* 8, 533-545), sterol carrier protein-2 (Colles, S. M. *et al.* 1995, *Lipids* 30, 795-803), cholesterol 7α-monooxygenase (Kai, M. *et al.* 1995, *Lipid Res.* 36,

367-374), cholesterol oxidase (Ishizaki, T. *et al.* 1991, *J. Bacteriol.* 171, 596-601), cholesterol dehydrogenase (Horinouchi, S. *et al.* 1991, *Apppl. Environ. Microbiol.* 57, 1386-1393), bile-salt-activated lipase precursor (cholesterol esterase) (Nilsson, J. *et al.* 1990, *Eur. J. Biochem.* 192, 543-550), and acyl-CoA cholesterol acyltransferase (Pape, M. E. *et al.* 1995, *J. Lipid Res.* 36, 823-838) we looked for the presence of the cholesterol recognition/interaction amino acid consensus pattern **-Z-$(X)_{0-5}$-Y-$(X)_{0-5}$-Q-** (SEQ ID NO:26) in these proteins. Table I shows that all these proteins, with the exception of sterol carrier protein-2, contain this amino acid consensus pattern. Proteins such as rat skeletal muscle alpha-actin, non-muscle and smooth muscle myosin light chain did not contain this cholesterol recognition/interaction consensus pattern. However, given any tyrosine there is a reasonably high probability that this consensus amino acid sequence will be found in many proteins. Indeed, a motif search through the various gene data banks indicated that this amino acid consensus pattern is present in various proteins. This is not surprising since it is known that the cholesterol/protein interaction plays a role not only in cholesterol transport and/or storage but also in protein stability, folding, and/or localization. Thus, it is possible that only in some proteins this consensus sequence will be functional. The strength and specificity of the interaction of a protein containing this consensus amino acid sequence with cholesterol may be due either to the presence of a certain microenvironment, or the location of the consensus sequence within the protein, or a specific conformation of the protein that allows the use of this amino acid sequence. In the latter case, it is also possible that the consensus sequence identified represents only a portion, maybe the core, of a larger motif to be identified.

Please amend the paragraph starting on line 33 of page 51 as follows:

In conclusion, the results presented herein demonstrate that PBR may have a channel-like function for cholesterol in the OMM. The steroidogenic pool of cholesterol, coming from various intracellular sources, is recognized by the cholesterol recognition/interaction amino acid consensus pattern **-Z-$(X)_{0-5}$-Y-$(X)_{0-5}$-Q-** (SEQ ID NO:26) present in the carboxy-terminus of PBR in the OMM. This pool of cholesterol enters in the OMM at the PBR sites where it remains without mixing with other membrane components. Ligand binding to the receptor induces the

release of this cholesterol. Considering that PBR has been shown to be associated with the voltage-dependent anion channel (Papadopoulos, V. 1998, *supra*), found in the outer/inner mitochondrial membrane contact sites, the release cholesterol could now directly access the P450scc in the IMM where it will be cleaved to pregnenolone, precursor of all steroids.